

1                   3. (As filed) The method according to claim 2, wherein prior to analysis, the locus at  
2 which the or each allele is situated is amplified.

1                   4. (As filed) The method according to claim 3, wherein the amplification is by the PCR.

1                   5. (Amended) The method according to [any one of] claim[s] 1 [to 4],  
2 wherein the locus at which the or each allele is situated comprises microsatellite repeats of  
3 variable length.

1                   6. (Amended) The method according to claim 3 [or claim 4], wherein the  
2 amplification is performed using a pair of primers for each allele, wherein each primer in a pair  
3 hybridizes under suitably stringent conditions to a region either side of the microsatellite  
4 repeats.

1                   7. (Amended) The method according to [any one of] claim[s] 1 [to 6],  
2 wherein the allele for identification is D4S3032\*5.

1                   8. (Amended) The method according to [any one of] claim[s] 1 [to 6],  
2 wherein the allele for identification is D4S2921\*13.

1                   9. (Amended) The method according to [any one of] claim[s] 1 [to 6],  
2 wherein the alleles for identification are D4S3032\*5 and D4S2921\*13.

1                   10. (Amended) The method according to [any one of] claim[s] 3 [to 9],  
2 wherein the analysis is carried out by size separation of amplification products.

1                   11. (As filed) The method according to claim 10, wherein the primers in the pair of  
2 primers comprise the oligonucleotide sequences identified by SEQ ID NO: 1 and SEQ ID NO: 2 or substantially  
3 similar sequences, for D4S3032\*5; or identified by SEQ ID NO: 3 and SEQ ID NO: 4 or substantially similar  
4 sequences, for D4S2921\*13; or both of the aforementioned pairs of primers for both of the aforementioned  
5 alleles.

1                   12. (As filed) A pair of oligonucleotide primers for amplification of an allele which is  
2 associated with asthma, which allele is situated at a locus in a region of chromosome 2 of up to 1 megabase in  
3 length, which region contains the locus D4S3032 and/or D4S2921.